STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/537,507
Source: PCT
Date Processed by STIC: 3/9/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**http://www.uspto.gov/ebc/efs/downloads/documents.htm**> , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):** U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/537,507

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1	Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2	Invalid Line Length	The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
3	Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
4	Non-ASCII	The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
5	Variable Length	Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6	PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
7	Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
8	Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence. <210> sequence id number <400> sequence id number 000
9	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
10	Invalid <213> Response	Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
11	Use of <220>	Sequence(s) ___ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
12	PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13	Misuse of n/Xaa	"n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid

PCT

RAW SEQUENCE LISTING DATE: 03/09/2006
PATENT APPLICATION: **US/10/537,507** TIME: 12:36:38

Input Set : **A:\PTO.KD.txt**
Output Set: **N:\CRF4\03092006\J537507.raw**

see item 2 on Error Summary Sheet

3 <110> APPLICANT: Aarhus Universitet
5 <120> TITLE OF INVENTION: Method for determining predisposition to manifestation of immune system
6 related diseases
8 <130> FILE REFERENCE: P 706 DK 02
C--> 10 <140> **CURRENT APPLICATION NUMBER: US/10/537,507**
C--> 10 <141> **CURRENT FILING DATE: 2005-06-03**
10 <160> NUMBER OF SEQ ID NOS: 8
12 <170> SOFTWARE: PatentIn version 3.1
14 <210> SEQ ID NO: 1
15 <211> LENGTH: 671
16 <212> TYPE: PRT
17 <213> ORGANISM: Homo sapiens; mature MASP-2
19 <400> SEQUENCE: 1

Does Not Comply
Corrected Diskette Needed

pp 3-5

```
21 Thr Pro Leu Gly Pro Lys Trp Pro Glu Pro Val Phe Gly Arg Leu Ala
22 1               5                  10                  15
25 Ser Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp Gln Glu Arg Arg Trp
26             20                  25                  30
29 Thr Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His
30         35                  40                  45
33 Phe Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu
34     50                  55                  60
37 Ser Ser Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr
38 65                  70                  75                  80
41 Asp Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser
42                 85                  90                  95
45 Ser Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe
46             100                 105                 110
49 Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln
50         115                 120                 125
53 Val Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His
54     130                 135                 140
57 Leu Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly Tyr Val Leu His Arg
58 145                 150                 155                 160
61 Asn Lys Arg Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gln
62                 165                 170                 175
65 Arg Ser Gly Glu Leu Ser Ser Pro Glu Tyr Pro Arg Pro Tyr Pro Lys
66             180                 185                 190
69 Leu Ser Ser Cys Thr Tyr Ser Ile Ser Leu Glu Glu Gly Phe Ser Val
70         195                 200                 205
73 Ile Leu Asp Phe Val Glu Ser Phe Asp Val Glu Thr His Pro Glu Thr
74     210                 215                 220
77 Leu Cys Pro Tyr Asp Phe Leu Lys Ile Gln Thr Asp Arg Glu Glu His
78 225                 230                 235                 240
```

RAW SEQUENCE LISTING DATE: 03/09/2006
PATENT APPLICATION: US/10/537,507 TIME: 12:36:38

Input Set : A:\PTO.KD.txt
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```
81 Gly Pro Phe Cys Gly Lys Thr Leu Pro His Arg Ile Glu Thr Lys Ser
82                 245                 250                 255
85 Asn Thr Val Thr Ile Thr Phe Val Thr Asp Glu Ser Gly Asp His Thr
86             260                 265                 270
89 Gly Trp Lys Ile His Tyr Thr Ser Thr Ala Gln Pro Cys Pro Tyr Pro
90         275                 280                 285
93 Met Ala Pro Pro Asn Gly His Val Ser Pro Val Gln Ala Lys Tyr Ile
94     290                 295                 300
97 Leu Lys Asp Ser Phe Ser Ile Phe Cys Glu Thr Gly Tyr Glu Leu Leu
98 305                 310                 315                 320
101 Gln Gly His Leu Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp
102                 325                 330                 335
105 Gly Ser Trp Asp Arg Pro Met Pro Ala Cys Ser Ile Val Asp Cys Gly
106             340                 345                 350
109 Pro Pro Asp Asp Leu Pro Ser Gly Arg Val Glu Tyr Ile Thr Gly Pro
110         355                 360                 365
113 Gly Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu Thr
114     370                 375                 380
117 Phe Tyr Thr Met Lys Val Asn Asp Gly Lys Tyr Val Cys Glu Ala Asp
118 385                 390                 395                 400
121 Gly Phe Trp Thr Ser Ser Lys Gly Glu Lys Ser Leu Pro Val Cys Glu
122                 405                 410                 415
125 Pro Val Cys Gly Leu Ser Ala Arg Thr Thr Gly Gly Arg Ile Tyr Gly
126             420                 425                 430
129 Gly Gln Lys Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Ile Leu
130         435                 440                 445
133 Gly Gly Thr Thr Ala Ala Gly Ala Leu Leu Tyr Asp Asn Trp Val Leu
134     450                 455                 460
137 Thr Ala Ala His Ala Val Tyr Glu Gln Lys His Asp Ala Ser Ala Leu
138 465                 470                 475                 480
141 Asp Ile Arg Met Gly Thr Leu Lys Arg Leu Ser Pro His Tyr Thr Gln
142                 485                 490                 495
145 Ala Trp Ser Glu Ala Val Phe Ile His Glu Gly Tyr Thr His Asp Ala
146             500                 505                 510
149 Gly Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Asn Asn Lys Val Val
150         515                 520                 525
153 Ile Asn Ser Asn Ile Thr Pro Ile Cys Leu Pro Arg Lys Glu Ala Glu
154     530                 535                 540
157 Ser Phe Met Arg Thr Asp Asp Ile Gly Thr Ala Ser Gly Trp Gly Leu
158 545                 550                 555                 560
161 Thr Gln Arg Gly Phe Leu Ala Arg Asn Leu Met Tyr Val Asp Ile Pro
162                 565                 570                 575
165 Ile Val Asp His Gln Lys Cys Thr Ala Ala Tyr Glu Lys Pro Pro Tyr
166             580                 585                 590
169 Pro Arg Gly Ser Val Thr Ala Asn Met Leu Cys Ala Gly Leu Glu Ser
170         595                 600                 605
173 Gly Gly Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe
174     610                 615                 620
177 Leu Asp Ser Glu Thr Glu Arg Trp Phe Val Gly Gly Ile Val Ser Trp
```

RAW SEQUENCE LISTING DATE: 03/09/2006
PATENT APPLICATION: US/10/537,507 TIME: 12:36:38

Input Set : A:\PTO.KD.txt
Output Set: N:\CRF4\03092006\J537507.raw

```
178 625                 630                 635                 640
181 Gly Ser Met Asn Cys Gly Glu Ala Gly Gln Tyr Gly Val Tyr Thr Lys
182                 645                 650                 655
185 Val Ile Asn Tyr Ile Pro Trp Ile Glu Asn Ile Ile Ser Asp Phe
186             660                 665                 670
189 <210> SEQ ID NO: 2
190 <211> LENGTH: 170
191 <212> TYPE: PRT
192 <213> ORGANISM: mature MAp-19 (human)
194 <400> SEQUENCE: 2
196 Thr Pro Leu Gly Pro Lys Trp Pro Glu Pro Val Phe Gly Arg Leu Ala
197 1               5                   10                  15
200 Ser Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp Gln Glu Arg Arg Trp
201             20                  25                  30
204 Thr Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His
205         35                  40                  45
208 Phe Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu
209     50                  55                  60
212 Ser Ser Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr
213 65                  70                  75                  80
216 Asp Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser
217                 85                  90                  95
220 Ser Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe
221             100                 105                 110
224 Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln
225         115                 120                 125
228 Val Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His
229     130                 135                 140
232 Leu Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly Tyr Val Leu His Arg
233 145                 150                 155                 160
236 Asn Lys Arg Thr Cys Ser Glu Gln Ser Leu
237                 165                 170
240 <210> SEQ ID NO: 3
241 <211> LENGTH: 2061
242 <212> TYPE: DNA
243 <213> ORGANISM: cDNA MASP-2
245 <400> SEQUENCE: 3
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Invalid <213> response. See item 10 on Error Summary Sheet.

```
246 atgaggctgc tgaccctcct gggccttctg tgtggctcgg tggccacccc cttgggcccg    60
248 aagtggcctg aacctgtgtt cgggcgcctg gcatcccccg gctttccagg ggagtatgcc   120
250 aatgaccagg agcggcgctg gaccctgact gcacccccgg gctaccgcct gcgcctctac   180
252 ttcacccact tcgacctgga gctctcccac ctctgcgagt acgacttcgt caagctgagc   240
254 tcgggggcca aggtgctggc cacgctgtgc gggcaggaga gcacagacac ggagcgggcc   300
256 cctggcaagg acactttcta ctcgctgggc tccagcctgg acattacctt ccgctccgac   360
258 tactccaacg agaagccgtt cacggggttc gaggccttct atgcagccga ggacattgac   420
260 gagtgccagg tggccccggg agaggcgccc acctgcgacc accactgcca caaccacctg   480
262 ggcggtttct actgctcctg ccgcgcaggc tacgtcctgc accgtaacaa gcgcacctgc   540
264 tcagccctgt gctccggcca ggtcttcacc cagaggtctg gggagctcag cagccctgaa   600
266 tacccacggc cgtatcccaa actctccagt tgcacttaca gcatcagcct ggaggagggg   660
268 ttcagtgtca ttctggactt tgtggagtcc ttcgatgtgg agacacaccc tgaaaccctg   720
```

RAW SEQUENCE LISTING DATE: 03/09/2006
PATENT APPLICATION: US/10/537,507 TIME: 12:36:38

Input Set : A:\PTO.KD.txt
Output Set: N:\CRF4\03092006\J537507.raw

270 tgtccctacg actttctcaa gattcaaaca gacagagaag aacatggccc attctgtggg 780
272 aagacattgc cccacaggat tgaaacaaaa agcaacacgg tgaccatcac ctttgtcaca 840
274 gatgaatcag gagaccacac aggctggaag atccactaca cgagcacagc gcagccttgc 900
276 ccttatccga tggcgccacc taatggccac gtttcacctg tgcaagccaa atacatcctg 960
278 aaagacagct tctccatctt ttgcgagact ggctatgagc ttctgcaagg tcacttgccc 1020
280 ctgaaatcct ttactgcagt ttgtcagaaa gatggatctt gggaccggcc aatgcccgcg 1080
282 tgcagcattg ttgactgtgg ccctcctgat gatctaccca gtggccgagt ggagtacatc 1140
284 acaggtcctg gagtgaccac ctacaaagct gtgattcagt acagctgtga agagaccttc 1200
286 tacacaatga aagtgaatga tggtaaatat gtgtgtgagg ctgatggatt ctggacgagc 1260
288 tccaaaggag aaaaatcact cccagtctgt gagcctgttt gtggactatc agcccgcaca 1320
290 acaggagggc gtatatatgg agggcaaaag gcaaaacctg gtgattttcc ttggcaagtc 1380
292 ctgatattag gtggaaccac agcagcaggt gcacttttat atgacaactg ggtcctaaca 1440
294 gctgctcatg ccgtctatga gcaaaaacat gatgcatccg ccctggacat tcgaatgggc 1500
296 accctgaaaa gactatcacc tcattataca caagcctggt ctgaagctgt ttttatacat 1560
298 gaaggttata ctcatgatgc tggctttgac aatgacatag cactgattaa attgaataac 1620
300 aaagttgtaa tcaatagcaa catcacgcct atttgtctgc caagaaaaga agctgaatcc 1680
302 tttatgagga cagatgacat tggaactgca tctggatggg gattaaccca aaggggtttt 1740
304 cttgctagaa atctaatgta tgtcgacata ccgattgttg accatcaaaa atgtactgct 1800
306 gcatatgaaa agccacccta tccaagggga agtgtaactg ctaacatgct ttgtgctggc 1860
308 ttagaaagtg ggggcaagga cagctgcaga ggtgacagcg gaggggcact ggtgtttcta 1920
310 gatagtgaaa cagagaggtg gtttgtggga ggaatagtgt cctggggttc catgaattgt 1980
312 ggggaagcag gtcagtatgg agtctacaca aaagttatta actatattcc ctggatcgag 2040
314 aacataatta gtgattttta a 2061
317 <210> SEQ ID NO: 4
318 <211> LENGTH: 558
319 <212> TYPE: DNA
320 <213> ORGANISM: cDNA MAp-19 same error
322 <400> SEQUENCE: 4
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325 aagtggcctg aacctgtgtt cgggcgcctg gcatcccccg gctttccagg ggagtatgcc 120
327 aatgaccagg agcggcgctg gaccctgact gcacccccgg gctaccgcct gcgcctctac 180
329 ttcacccact tcgacctgga gctctcccac ctctgcgagt acgacttcgt caagctgagc 240
331 tcgggggcca aggtgctggc cacgctgtgc gggcaggaga gcacagacac ggagcgggcc 300
333 cctggcaagg acactttcta ctcgctgggc tccagcctgg acattacctt ccgctccgac 360
335 tactccaacg agaagccgtt cacggggttc gaggccttct atgcagccga ggacattgac 420
337 gagtgccagg tggccccggg agaggcgccc acctgcgacc accactgcca caaccacctg 480
339 ggcggtttct actgctcctg ccgcgcaggc tacgtcctgc accgtaacaa gcgcacctgc 540
341 tcagagcaga gcctctag 558
344 <210> SEQ ID NO: 5
345 <211> LENGTH: 21
346 <212> TYPE: DNA
347 <213> ORGANISM: upper PCR primer
349 <400> SEQUENCE: 5
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353 <210> SEQ ID NO: 6
354 <211> LENGTH: 21
355 <212> TYPE: DNA
356 <213> ORGANISM: lower PCR primer
358 <400> SEQUENCE: 6

RAW SEQUENCE LISTING DATE: 03/09/2006
PATENT APPLICATION: **US/10/537,507** TIME: 12:36:38

Input Set : **A:\PTO.KD.txt**
Output Set: **N:\CRF4\03092006\J537507.raw**

359 ctcggctgca tagaaggcct c 21
362 <210> SEQ ID NO: 7
363 <211> LENGTH: 21
364 <212> TYPE: DNA
365 <213> ORGANISM: upper PCR primer
367 <400> SEQUENCE: 7
368 ccagaccttt ggaaagttag c 21
371 <210> SEQ ID NO: 8
372 <211> LENGTH: 21
373 <212> TYPE: DNA
374 <213> ORGANISM: lower PCR primer
376 <400> SEQUENCE: 8
377 ggctcaagtt ccaagtattg c 21

VERIFICATION SUMMARY DATE: 03/09/2006
PATENT APPLICATION: **US/10/537,507** TIME: 12:36:39

Input Set : **A:\PTO.KD.txt**
Output Set: **N:\CRF4\03092006\J537507.raw**

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date